

#7
nb
09/28/01

OIEP

RAW SEQUENCE LISTING

DATE: 07/16/2001

PATENT APPLICATION: US/09/724,126A

TIME: 14:15:51

Input Set : A:\35966Aseq.txt

Output Set: N:\CRF3\07162001\I724126A.raw

P.S

ENTERED

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5 <110> APPLICANT: Han, Hui-Quan
6 Kwak, Keith
9 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
11 <130> FILE REFERENCE: 01017/35966A
13 <140> CURRENT APPLICATION NUMBER: US 09/724,126A
14 <141> CURRENT FILING DATE: 2000-11-28
16 <150> PRIOR APPLICATION NUMBER: US 60/187,211
17 <151> PRIOR FILING DATE: 1999-03-01
19 <160> NUMBER OF SEQ ID NOS: 29
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 6308
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (696)..(5942)
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37 ccaaaggctt atcatctgtc ttccacttat ccaacaagct gctatggcca ctgcctgtgc 180
39 cgcacctgga accaccgcca gccccactac tgccctccact accactgggt ctcccaccct 240
41 gatcagctgc ttgctgctgc catcttatcc gcttctgcct gttctgagta aatgtataca 300
43 caccctggaa accaccattc tactttctgt gtctatgaat ttgactactc tagctggatc 360
45 ccgagctttt ttgtacacat gtgcaagtgc ccacggggta gaatcctaaa aatagaagat 420
47 gtatgcaaca gttcccagca ccaaaccagc atatacaacc attcagctac caagagctac 480
49 gcctgataaa ttagagggga aaaaaaaaaa ctccagtcctc ttcacgtcgt gacgcttgct 540
51 tccgggaagc gggccggaag ccactcctcg agtctgcgtc aaaccgcact tcaggggccc 600
53 tcgtaaaagt gtcgtccctg tctctccgac cggccacagg tttccgcttg cctctggccc 660
55 ggggtcggca actgcaggcg tcagtttccc tcaag atg gcg gag gag gct 713
56 Met Ala Asp Glu Glu Ala
57 1 5
59 gga ggt act gag agg atg gaa atc agc gcg gag tta ccc cag acc cct 761
60 Gly Gly Thr Glu Arg Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro
61 10 15 20
63 cag cgt ctg gca tct tgg tgg gat cag caa gtt gat ttt tat act gct 809
64 Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala
65 25 30 35
67 ttc ttg cat cat ttg gca caa ttg gtg cca gaa att tac ttt gct gaa 857
68 Phe Leu His His Leu Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu
69 40 45 50
71 atg gac cca gac ttg gaa aag cag gag gaa agt gta caa atg tca ata 905
72 Met Asp Pro Asp Leu Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile
73 55 60 65 70
75 ttc act cca ctg gaa tgg tac tta ttt gga gaa gat cca gat att tgc 953
76 Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys
77 75 80 85

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84	Phe	Lys	Ser	Gly	Glu	Thr	Thr	Tyr	Ser	Cys	Arg	Asp	Cys	Ala	Ile	Asp	
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88	Pro	Thr	Cys	Val	Leu	Cys	Met	Asp	Cys	Phe	Gln	Asp	Ser	Val	His	Lys	
89			120				125					130					
91	aat	cat	cgt	tac	aag	atg	cat	act	tct	act	gga	gga	ggg	ttc	tgt	gac	1145
92	Asn	His	Arg	Tyr	Lys	Met	His	Thr	Ser	Thr	Gly	Gly	Gly	Phe	Cys	Asp	
93	135					140					145				150		
95	tgt	gga	gac	aca	gag	gca	tgg	aaa	act	ggc	cct	ttt	tgt	gta	aat	cat	1193
96	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Thr	Gly	Pro	Phe	Cys	Val	Asn	His	
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101				170				175					180				
103	aat	gaa	gag	gta	att	gtc	caa	gcc	agg	aaa	ata	ttt	cct	tca	gtg	ata	1289
104	Asn	Glu	Glu	Val	Ile	Val	Gln	Ala	Arg	Lys	Ile	Phe	Pro	Ser	Val	Ile	
105			185				190					195					
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108	Lys	Tyr	Val	Val	Glu	Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	
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111	cct	gaa	ctc	cag	ata	agg	gag	aaa	aat	gaa	aga	tac	tat	tgt	gtc	ctt	1385
112	Pro	Glu	Leu	Gln	Ile	Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	
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117	ttc	aat	gat	gaa	cac	cat	tca	tat	gac	cac	gtc	ata	tac	agc	cta	caa	1433
118	Phe	Asn	Asp	Glu	His	His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	
119				235				240				245					
121	aga	gct	ctt	gac	tgt	gag	ctc	gca	gag	gcc	cag	ttg	cat	acc	act	gcc	1481
122	Arg	Ala	Leu	Asp	Cys	Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	
123				250				255				260					
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127	Ile	Asp	Lys	Glu	Gly	Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	
128			265				270					275					
130	tgc	cag	gaa	gca	aag	gaa	gat	ata	aag	agt	cat	tca	gaa	aat	gtc	tct	1577
131	Cys	Gln	Glu	Ala	Lys	Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	
132			280				285					290					
134	caa	cat	cca	ctt	cat	gta	gaa	gta	tta	cac	tca	gag	att	atg	gct	cat	1625
135	Gln	His	Pro	Leu	His	Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	
136	295					300					305				310		
138	cag	aaa	ttt	gct	ttg	cgt	ctt	ggt	tcc	tgg	atg	aac	aaa	att	atg	agc	1673
139	Gln	Lys	Phe	Ala	Leu	Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	
140				315				320				325					
142	tat	tca	agt	gac	ttt	agg	cag	atc	ttt	tgc	caa	gca	tgc	ctt	aga	gaa	1721
143	Tyr	Ser	Ser	Asp	Phe	Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	
144				330				335				340					
146	gaa	cct	gac	tcg	gag	aat	ccc	tgt	ctc	ata	agc	agg	tta	atg	ctt	tgg	1769

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150	gat	gca	aag	ctt	tat	aaa	ggt	gcc	cgt	aag	atc	ctt	cat	gaa	ttg	atc	1817
151	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	
152		360					365					370					
154	ttc	agc	agt	ttt	ttt	atg	gag	atg	gaa	tac	aaa	aaa	ctc	ttt	gct	atg	1865
155	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	
156	375					380					385					390	
158	gaa	ttt	gtg	aag	tat	tat	aaa	caa	ctg	cag	aaa	gaa	tat	atc	agt	gat	1913
159	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	
160				395						400					405		
162	gat	cat	gac	aga	agt	atc	tct	ata	act	gca	ctt	tca	ggt	cag	atg	ttt	1961
163	Asp	His	Asp	Arg	Ser	Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	
164			410						415					420			
166	act	ggt	cct	act	ctg	gct	cga	cat	ctt	att	gaa	gag	cag	aat	ggt	atc	2009
167	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	
168		425					430						435				
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171	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	
172		440					445					450					
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177	455				460					465					470		
179	aga	gta	tat	gca	gta	ata	tgt	gac	cta	aag	tat	atc	ctg	atc	agc	aaa	2153
180	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	
181				475					480					485			
183	ccc	aca	ata	tgg	aca	gaa	aga	tta	aga	atg	cag	ttc	ctt	gaa	ggt	ttt	2201
184	Pro	Thr	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	
185			490						495				500				
188	cga	tct	ttt	ttg	aag	att	ctt	acc	tgt	atg	cag	gga	atg	gaa	gaa	atc	2249
189	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	
190			505					510					515				
192	cga	aga	cag	ggt	ggg	caa	cac	att	gaa	gtg	gat	cct	gat	tgg	gag	gct	2297
193	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val	Asp	Pro	Asp	Trp	Glu	Ala	
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197	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn	Ile	Leu	Leu	Met	Phe	Gln	
198	535				540					545					550		
200	gag	tgg	tgt	gct	tgt	gat	gaa	gaa	ctc	tta	ctt	gtg	gct	tat	aaa	gaa	2393
201	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Glu	Leu	Leu	Val	Ala	Tyr	Lys	Glu		
202				555					560					565			
204	tgt	cac	aaa	gct	gtg	atg	agg	tgc	agt	acc	agt	ttc	ata	tct	agt	agc	2441
205	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	
206			570					575					580				
208	aag	aca	gta	gta	caa	tcg	tgt	gga	cat	agt	ttg	gaa	aca	aag	tcc	tac	2489
209	Lys	Thr	Val	Val	Gln	Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	
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218	615 620 625 630			
220	ctg cat gaa ttt gtg tct ttt gag gac ttt caa gta gag gta cta gtg	2633		
221	Leu His Glu Phe Val Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val			
222	635 640 645			
224	gaa tat cct tta cgt tgt ctg gtg ttg gtt gcc cag gtt gtt gct gag	2681		
225	Glu Tyr Pro Leu Arg Cys Leu Val Leu Val Ala Gln Val Val Ala Glu			
226	650 655 660			
228	atg tgg cga aga aat gga ctg tct ctt att agc cag gtg ttt tat tac	2729		
229	Met Trp Arg Arg Asn Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr			
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233	caa gat gtt aag tgc aga gaa gaa atg tat gat aaa gat atc atc atg	2777		
234	Gln Asp Val Lys Cys Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met			
235	680 685 690			
237	ctt cag att ggt gca tct tta atg gat ccc aat aag ttc ttg tta ctg	2825		
238	Leu Gln Ile Gly Ala Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu			
239	695 700 705 710			
241	gta ctt cag agg tat gaa ctt gcc gag gct ttt aac aag acc ata tct	2873		
242	Val Leu Gln Arg Tyr Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser			
243	715 720 725			
245	aca aaa gac cag gat ttg att aaa caa tat aat aca cta ata gaa gaa	2921		
246	Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu			
247	730 735 740			
250	atg ctt cag gtc ctc atc tat att gtg ggt gag cgt tat gta cct gga	2969		
251	Met Leu Gln Val Leu Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly			
252	745 750 755			
254	gtg gga aat gtg acc aaa gaa gag gtc aca atg aga gaa atc att cac	3017		
255	Val Gly Asn Val Thr Lys Glu Glu Val Thr Met Arg Glu Ile Ile His			
256	760 765 770			
258	ttg ctt tgc att gaa ccc atg cca cac agt gcc att gcc aaa aat tta	3065		
259	Leu Leu Cys Ile Glu Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu			
260	775 780 785 790			
262	cct gag aat gaa aat aat gaa act ggc tta gag aat gtc ata aac aaa	3113		
263	Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys			
264	795 800 805			
266	gtg gcc aca ttt aag aaa cca ggt gta tca ggc cat gga gtt tat gaa	3161		
267	Val Ala Thr Phe Lys Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu			
268	810 815 820			
270	cta aaa gat gaa tca ctg aaa gac ttc aat atg tac ttt tat cat tac	3209		
271	Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr			
272	825 830 835			
274	tcc aaa acc cag cat agc aag gct gaa cat atg cag aag aaa agg aga	3257		
275	Ser Lys Thr Gln His Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg			
276	840 845 850			
278	aaa caa gaa aac aaa gat gaa gca ttg ccg cca cca cca cct cct gaa	3305		
279	Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro Pro Pro Pro Pro Pro Glu			
280	855 860 865 870			

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284					875					880					885		
286	atg	atg	tac	att	ctc	agg	acc	gta	ttt	gag	cgg	gca	ata	gac	aca	gat	3401
287	Met	Met	Tyr	Ile	Leu	Arg	Thr	Val	Phe	Glu	Arg	Ala	Ile	Asp	Thr	Asp	
288				890					895					900			
291	tct	aac	ttg	tgg	acc	gaa	ggg	atg	ctc	caa	atg	gct	ttt	cat	att	ctg	3449
292	Ser	Asn	Leu	Trp	Thr	Glu	Gly	Met	Leu	Gln	Met	Ala	Phe	His	Ile	Leu	
293			905					910					915				
295	gca	ttg	ggt	tta	cta	gaa	gag	aag	caa	cag	ctt	caa	aaa	gct	cct	gaa	3497
296	Ala	Leu	Gly	Leu	Leu	Glu	Glu	Lys	Gln	Gln	Leu	Gln	Lys	Ala	Pro	Glu	
297		920					925					930					
299	gaa	gaa	gta	aca	ttt	gac	ttt	tat	cat	aag	gct	tca	aga	ttg	gga	agt	3545
300	Glu	Glu	Val	Thr	Phe	Asp	Phe	Tyr	His	Lys	Ala	Ser	Arg	Leu	Gly	Ser	
301	935				940					945					950		
303	tca	gcc	atg	aat	ata	caa	atg	ctt	ttg	gaa	aaa	ctc	aaa	gga	att	ccc	3593
304	Ser	Ala	Met	Asn	Ile	Gln	Met	Leu	Leu	Glu	Lys	Leu	Lys	Gly	Ile	Pro	
305				955						960					965		
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308	Gln	Leu	Glu	Gly	Gln	Lys	Asp	Met	Ile	Thr	Trp	Ile	Leu	Gln	Met	Phe	
309				970				975					980				
312	gac	aca	gtg	aag	cga	tta	aga	gaa	aaa	tct	tgt	tta	att	gta	gca	acc	3689
313	Asp	Thr	Val	Lys	Arg	Leu	Arg	Glu	Lys	Ser	Cys	Leu	Ile	Val	Ala	Thr	
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317	Thr	Ser	Gly	Ser	Glu	Ser	Ile	Lys	Asn	Asp	Glu	Ile	Thr	His	Asp		
318		1000					1005					1010					
320	aaa	gaa	aaa	gca	gaa	cga	aaa	aga	aaa	gct	gaa	gct	gct	agg	cta		3779
321	Lys	Glu	Lys	Ala	Glu	Arg	Lys	Arg	Lys	Ala	Glu	Ala	Ala	Arg	Leu		
322		1015					1020					1025					
324	cat	cgc	cag	aag	atc	atg	gct	cag	atg	tct	gcc	tta	cag	aaa	aac		3824
325	His	Arg	Gln	Lys	Ile	Met	Ala	Gln	Met	Ser	Ala	Leu	Gln	Lys	Asn		
326		1030					1035					1040					
328	ttc	att	gaa	act	cat	aaa	ctc	atg	tat	gac	aat	aca	tca	gaa	atg		3869
329	Phe	Ile	Glu	Thr	His	Lys	Leu	Met	Tyr	Asp	Asn	Thr	Ser	Glu	Met		
330		1045					1050					1055					
332	cct	ggg	aaa	gaa	gat	tcc	att	atg	gag	gaa	gag	agc	acc	cca	gca		3914
333	Pro	Gly	Lys	Glu	Asp	Ser	Ile	Met	Glu	Glu	Glu	Ser	Thr	Pro	Ala		
334		1060					1065					1070					
336	gtc	agt	gac	tac	tct	aga	att	gct	ttg	ggt	cct	aaa	cgg	ggt	cca		3959
337	Val	Ser	Asp	Tyr	Ser	Arg	Ile	Ala	Leu	Gly	Pro	Lys	Arg	Gly	Pro		
338		1075					1080					1085					
340	tct	gtt	act	gaa	aag	gag	gtg	ctg	acg	tgc	atc	ctt	tgc	caa	gaa		4004
341	Ser	Val	Thr	Glu	Lys	Glu	Val	Leu	Thr	Cys	Ile	Leu	Cys	Gln	Glu		
342		1090					1095					1100					
344	gaa	cag	gag	gtg	aaa	ata	gaa	aat	aat	gcc	atg	gta	tta	tcg	gcc		4049
345	Glu	Gln	Glu	Val	Lys	Ile	Glu	Asn	Asn	Ala	Met	Val	Leu	Ser	Ala		
346		1105					1110					1115					
349	tgt	gtc	cag	aaa	tct	act	gcc	tta	acc	cag	cac	agg	gga	aaa	ccc		4094

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

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L:2834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18